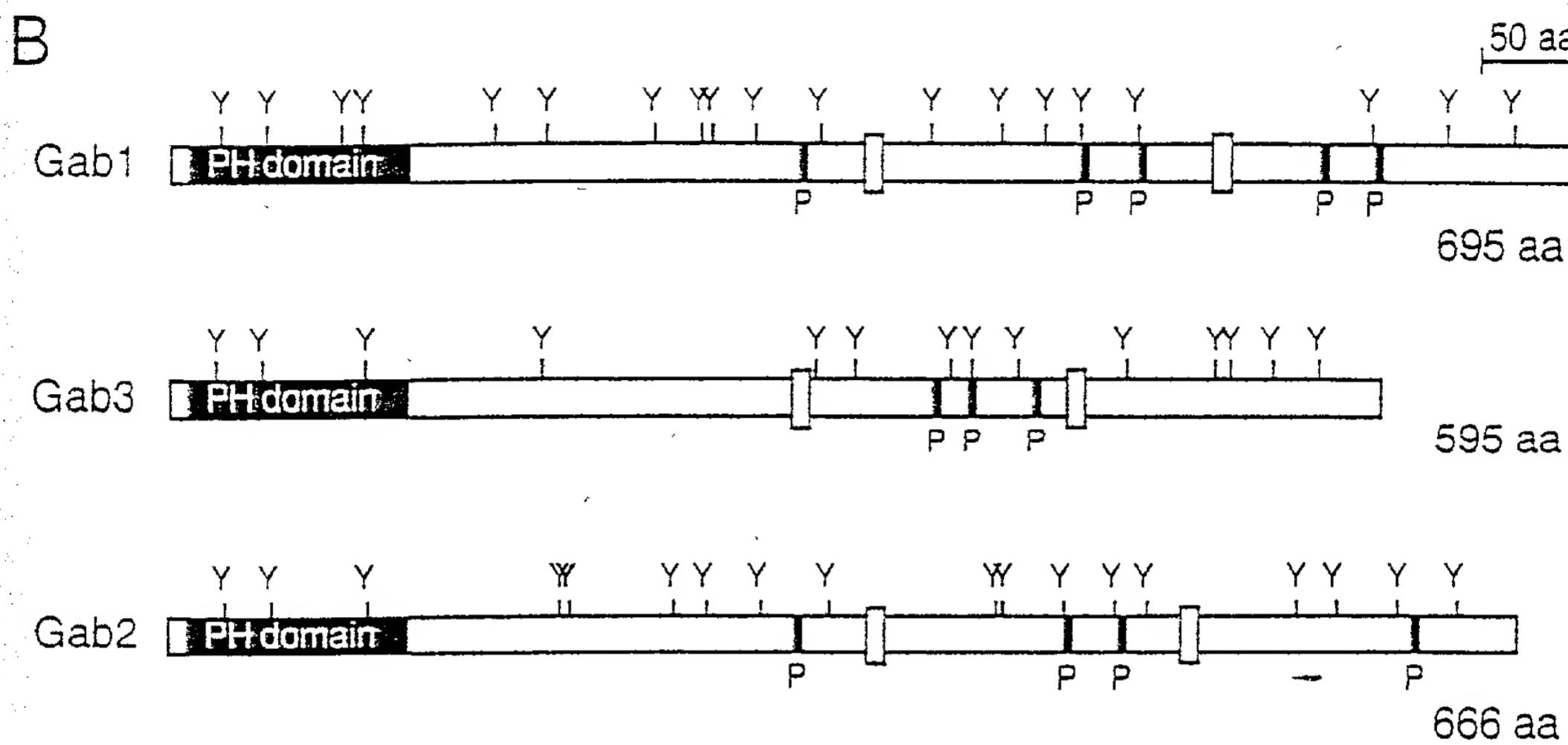


A

Human	MSAGDAVCTGWLVKSPPERKLQRYAWRKRWFVLRRGRMSGNPDVLEYYRNKHSSKPIRVI	60
Murine	MSTGDTVCMGWLIKSPPERKLQRYAWRKRWFVLRRGRMSGNPDVLEYYRNKHSNKPIRVI	60
::***:*****:*****:*****:*****:*****:*****:*****:*****:*****		
Human	DLSECAVWKHVGPSFVRKEFQNNFVFIVKTTSRFTYLVAKTEQEMQVWVHSISQVCNLGH	120
Murine	DLSECTVWKHAGPGFIRKEFQKNFVFIVKTTSRFTYLVAKTEEMQVWVHSISQVCNFSH	120
*****:*****.**.*:*****:*****:*****:*****:*****:*****:*****:.*		
Human	LEDGADSMESLSYTPSSLQPSSASSLLTAHAASSSLPRDDPNTNAVATEETRSESELLFL	180
Murine	LEDGADSMESLSHMPSSFQPSPASSLHTVHVANSALLKDDGNTNSVVTETRRESEFLFL	180
*****:***:***.*** *.*.*.*:*** ***:*.***** ***:***		
Human	PDYLVLSNCETGRLHHTSLPTRCDSWSNSDRSLEQASFDDVFVDCLQPLPSSHVLVHPSCH	240
Murine	PDYLILSNCETGRLHHASLPTRCDSWSNSNHSLAQTSFDDVFLDGLQPFISNNLVHPLHH	240
*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****		
Human	GSGAQEVPSRPQAALIWSREINGPPRDHLSSPLLESSLSSTIQVDKNQGSLPCGAKEL	300
Murine	GKVSQDFPSIRPQASLIWNREINGPSRNLMSSPLLESSLNPTVHVEEKQVSLPSGVKEL	300
. ::..** ****:***.*****.*: :*****:*****..*:***:***.***		
Human	DIMSNT PPPRPKPSHL SERRQEE--WSTHSGSKKPECTLVPRIISLSGLDNMRTWKADV	358
Murine	NIMSN PPPRPKPSYL SEQRQDQPLLTGHSSNKPGYTMVPRRIISLSGLDHVGSKGDV	360
:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****		
Human	EGQSLRHRDKRLSLNLPCKF SPMY PTASASIEDSYV PM QAGASGLGPHCSPDDY IP MN	418
Murine	QSQSLRHRDKRLSLNLPCKF SP YPTASPSAEDSYV PM SPKGTAELRPHCSQDDY IP MS	420
:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****		
Human	SGSISSPL PELPAN LE PPVNRDLK QRKSRPPLDRLNLSIIREHASLTRRTVPCSR	478
Murine	S----SML PELPAD LE PPVNRNLK QRKSRPPLD SRNL STIQEHTSLRTYTVPCNRT	476
* * *****:*****:*****:*****:*****:*****:*****:*****:*****:*****		
Human	SFLSPERNGINSARFFAN PVSREDEES -----YIEMEEHRTASSLSSGALTWT	527
Murine	SFLSPQRNGINCARLF STPSEE EEEEEEEEE EKYIQMEEYGTVSSL RSRSALSWTK	536
*****:*****.**:*.** ..*:***:*****:*****.**:*****:*****.**		
Human	<u>SHP2</u>	<u>SHP2</u>
Murine	KFSLDYLA DNSASPAPMQ QKLLLSEEQRVDYVQVDEQKTQALQSTKQEW TDER QSKV	586
*****:*****:*****:*****:*****:*****:*****:*****:*****:*****		

Figure 1A



C

Gab3	MSTG--D-TVCMGWL IKSPP ERKLQRYAWRKRWFVLRRGR	37
Gab2	MSGGGGGDDVVCTGWL RKSP PEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VV CSGWL RKSPPEKKL KRYAWKRRWF VLRSGR	37
	*** * : . * * * * * * * * : * * : * * * * : : * * * : * * * * :	
Gab3	MSGNPDVLEYYRN KHSNKPIRVIDL SECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYYKNEH HSKKPLRI INLNLC EQVD -AGLTFNK	79
Gab1	LTGDPDVLEYYKND HAKKPIRI IDLNLC QVVD -AGLTFNK	76
	:. * : * * * * * * : * . * : * : * : * . * . * * * * : :	
Gab3	KEFQKNFVFIV KTT SRTFYL VAKT EEEMQVWVHSISQVCN	117
Gab2	KELQDSFVFD DIK T TS RTFYL VAE TEADMNKWVQSICQICG	119
Gab1	KEFENS YIFD INTIDRIFYL VAD SEEDMNK WVRC CICDICG	116
	** : . . . : * : * . * * * * * : * : * : * : * : . * . : * . :	

Figure 1B and C